

06/18/2007 - Monday				
Time	Type	Abstract #	Title	Speaker
730 - 830am	Breakfast	x	La Fonda Breakfast Buffet (TBD)	x
830 - 845	Intro	x	Welcome Intro	Gary Resnick
845 - 930	Keynote	FF0045	Finishing in the New DNA Sequencing Era	George Weinstock
930 - 950	Speaker 1	FF0042	Building Better Genomes	Jeremy Schmutz
950 - 1010	Speaker 2	FF0111	GEBA - A genomic encyclopedia of bacteria and archaea	Jonathan Eisen
1010 - 1040	Break	x	Beverages and snacks provided	x
1040 - 1100	Speaker 3	FF0080	Manual Sequencing Improvement of Bacterial Genomes	Aye Wollam
1100 - 1120	Speaker 4	FF0087	A High-Throughput cDNA Finishing Pipeline - <i>Bos Taurus</i> as a Model	Johar Ali
1120-1220	Panel Discussion	x	Panel Discussion	Chair - Johar Ali
1230 - 145pm	Lunch	x	Pecos Lunch Buffet (TBD)	x
200 - 220	Speaker 5	FF0088	Assembly and Finishing using 454 Sequencing Data (454)	Jim Knight
220 - 240	Speaker 6	FF0110	The Illumina Genome Analyzer System: Cost-effective, High Throughput Genomics Using Solexa DNA Sequencing Technology (Solexa)	Gary Schroth
240 - 300	Speaker 7	FF0099	Using a gigabase of short reads: leveraging paired end reads and color base encoding in the AB SOLiD TM sequencing system in finishing and SNP detection (Solid)	Fiona Hyland
300 - 400	Panel Discussion	x	Panel Discussion	Chair - Darren Grafham
400 - 430	Break	x	Beverages and snacks provided	x
430 - 600	Posters - odd #s	x	Poster Session	x
630 - 900pm	Meet & Greet Party	x	Meet & Greet Party - sponsored by Roche --- Food & Drinks	x
06/19/2007 - Tuesday				
Time	Type	Abstract #	Title	Speaker
730 - 830am	Breakfast	x	Santa Fe Breakfast Buffet (TBD)	x
830 - 845	Intro	x	Welcome Back Intro - Informatics	Jim Bristow
845 - 930	Keynote	FF0011	Automating the finishing process: dreams and realities	Mihai Pop
930 - 950	Speaker 1	FF0018	Celera Assembler: Adapting for the Future	Granger Sutton
950 - 1010	Speaker 2	FF0115	Charting and Sequencing Structural Variation using High-Resolution Paired-End Mapping (HR-PEM)	Jan Korbel
1010 -1040	Break	x	Beverages and snacks provided	x
1040 -1100	Speaker 3	FF0005	Assessment of 454 Sequencing Errors in Microbial Genomes	Stephan Trong
1100 -1120	Speaker 4	FF0026	New Sequencing Technologies and Hybrid Assemblies - A discussion on a shift in finishing paradigm: do we need to analyze each read?	Harindra Arachchi
1120 - 1220	Panel Discussion	x	Panel Discussion	Chair - Patrick Chain
1230 - 145pm	Lunch	x	La Fonda Lunch Buffet (TBD)	x
200-220	Speaker 5	FF0090	Transforming Genomes with New Sequencing Technology	Donna Muzny
220-240	Speaker 6	FF0039	De novo Hybrid 454 / Sanger Genome Assembly of <i>Phytophthora capsici</i>	Joann Mudge
240 - 300	Speaker 7	FF0032	Incorporating New Sequencing Technologies into Finishing Strategy	Sean Sykes
300 - 400	Panel Discussion	x	Panel Discussion	Chair - Donna Muzny
400 - 430	Break	x	Beverages, Wine & Cheese provided - sponsored by IDT & Edge	x
430 - 600	Posters - even #s	x	Poster Session with Wine & Cheese - sponsored by IDT & Edge	x
600 - bedtime	on your own	x	Dinner and night on your own - enjoy	x
06/20/2007 - Wednesday				
Time	Type	Abstract #	Title	Speaker
745 - 845am	Breakfast	x	Santa Fe Breakfast Buffet (TBD)	x
845 - 900	Intro	x	Welcome Back Intro - New Technologies	Paul Richardson
900 - 930	Speaker 1	FF0033d	New Amplification and Cloning Tools for Finishing Genomes	David Mead
930 - 950	Speaker 2	FF0076	Metagenomic Assembly QC	Alla Lapidus
950 -1020	Break	x	Beverages and snacks provided	x
1020 -1040	Speaker 3	FF0102	TaxSorter: A Solution to Metagenomic Projects	Li Liu
1040 -1100	Speaker 4	FF0065	Evaluation of New methods and Approaches for Comparative Metagenomic Studies	Emmanuel Mongodin
1100 -1200	Panel Discussion	x	Panel Discussion - New Technologies	Chair - Alla Lapidus
1200 - 130pm	Lunch & Close of meeting	x	La Fonda Lunch Buffet (?) End of meeting, enjoy lunch and Santa Fe	x